

09/582340

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## SEQUENCE LISTING

<110> INSERM  
INSTITUT CURIE  
CNRS

<120> Compositions and Methods using Lactadherin or Variants thereof

<130> Lactadherin

<140>

<141>

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 1934

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (61)..(1224)

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Met Pro Arg Pro Arg Leu Leu Ala Ala Leu Cys Gly Ala Leu Leu Cys  
1 5 10 15

gcc ccc agc ctc ctc gtc gcc ctg gat atc tgt tcc aaa aac ccc tgc 156  
Ala Pro Ser Leu Leu Val Ala Leu Asp Ile Cys Ser Lys Asn Pro Cys  
20 25 30

cac aac ggt ggt tta tgc gag gag att tcc caa gaa gtg cga gga gat 204  
His Asn Gly Gly Leu Cys Glu Glu Ile Ser Gln Glu Val Arg Gly Asp  
35 40 45

gtc ttc ccc tcg tac acc tgc acg tgc ctt aag ggc tac gcg ggc aac 252  
Val Phe Pro Ser Tyr Thr Cys Thr Cys Leu Lys Gly Tyr Ala Gly Asn  
50 55 60

cac tgt gag acg aaa tgt gtc gag cca ctg ggc atg gag aat ggg aac 300  
His Cys Glu Thr Lys Cys Val Glu Pro Leu Gly Met Glu Asn Gly Asn  
65 70 75 80

att gcc aac tca cag atc gcc gcc tca tct gtg cgt gtg acc ttc ttg 348  
Ile Ala Asn Ser Gln Ile Ala Ala Ser Ser Val Arg Val Thr Phe Leu  
85 90 95

Subcy

ggt ttg cag cat tgg gtc ccg gag ctg gcc cgc ctg aac cgc gca ggc	396
Gly Leu Gln His Trp Val Pro Glu Leu Ala Arg Leu Asn Arg Ala Gly	
100 105 110	
atg gtc aat gcc tgg aca ccc agc agc aat gac gat aac ccc tgg atc	444
Met Val Asn Ala Trp Thr Pro Ser Ser Asn Asp Asp Asn Pro Trp Ile	
115 120 125	
cag gtg aac ctg ctg cgg agg atg tgg gta aca ggt gtg gtg acg cag	492
Gln Val Asn Leu Leu Arg Arg Met Trp Val Thr Gly Val Val Thr Gln	
130 135 140	
ggt gcc agc cgc ttg gcc agt cat gag tac ctg aag gcc ttc aag gtg	540
Gly Ala Ser Arg Leu Ala Ser His Glu Tyr Leu Lys Ala Phe Lys Val	
145 150 155 160	
gcc tac agc ctt aat gga cac gaa ttc gat ttc atc cat gat gtt aat	588
Ala Tyr Ser Leu Asn Gly His Glu Phe Asp Phe Ile His Asp Val Asn	
165 170 175	
aaa aaa cac aag gag ttt gtg ggt aac tgg aac aaa aac gcg gtg cat	636
Lys Lys His Lys Glu Phe Val Gly Asn Trp Asn Lys Asn Ala Val His	
180 185 190	
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Val Asn Leu Phe Glu Thr Pro Val Glu Ala Gln Tyr Val Arg Leu Tyr	
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ccc acg agc tgc cac acg gcc tgc act ctg cgc ttt gag cta ctg ggc	732
Pro Thr Ser Cys His Thr Ala Cys Thr Leu Arg Phe Glu Leu Leu Gly	
210 215 220	
tgt gag ctg aac gga tgc gcc aat ccc ctg ggc ctg aag aat aac agc	780
Cys Glu Leu Asn Gly Cys Ala Asn Pro Leu Gly Leu Lys Asn Asn Ser	
225 230 235 240	
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Ile Pro Asp Lys Gln Ile Thr Ala Ser Ser Ser Tyr Lys Thr Trp Gly	
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Leu His Leu Phe Ser Trp Asn Pro Ser Tyr Ala Arg Leu Asp Lys Gln	
260 265 270	
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Gly Asn Phe Asn Ala Trp Val Ala Gly Ser Tyr Gly Asn Asp Gln Trp	
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ctg cag gtg gac ctg ggc tcc tgc aag gag gtg aca ggc atc atc acc	972
Leu Gln Val Asp Leu Gly Ser Ser Lys Glu Val Thr Gly Ile Ile Thr	
290 295 300	
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Gln Gly Ala Arg Asn Phe Gly Ser Val Gln Phe Val Ala Ser Tyr Lys	

305	310	315	320	
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Val Ala Tyr Ser Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro				
325		330	335	
agg act ggc agc agt aag atc ttc cct ggc aac tgg gac aac cac tcc				1116
Arg Thr Gly Ser Ser Lys Ile Phe Pro Gly Asn Trp Asp Asn His Ser				
340		345	350	
cac aag aag aac ttg ttt gag acg ccc atc ctg gct cgc tat gtg cgc				1164
His Lys Lys Asn Leu Phe Glu Thr Pro Ile Leu Ala Arg Tyr Val Arg				
355		360	365	
atc ctg cct gta gcc tgg cac aac cgc atc gcc ctg cgc ctg gag ctg				1212
Ile Leu Pro Val Ala Trp His Asn Arg Ile Ala Leu Arg Leu Glu Leu				
370		375	380	
ctg ggc tgt tag tggccacctg ccacccccag gtcttctgc tttccatggg				1264
Leu Gly Cys				
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cccgtgcct cttggcttct cagccccctt aaatcaccat agggctgggg actggggaag				1324
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<211> 387

<212> PRT

<213> Homo sapiens

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His Asn Gly Gly	Leu Cys Glu Glu Ile Ser Gln Glu Val Arg Gly Asp		
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Val Phe Pro Ser Tyr Thr Cys Thr Cys Leu Lys Gly Tyr Ala Gly Asn			
50	55	60	
His Cys Glu Thr Lys Cys Val Glu Pro Leu Gly Met Glu Asn Gly Asn			
65	70	75	80
Ile Ala Asn Ser Gln Ile Ala Ala Ser Ser Val Arg Val Thr Phe Leu			
85	90	95	
Gly Leu Gln His Trp Val Pro Glu Leu Ala Arg Leu Asn Arg Ala Gly			
100	105	110	
Met Val Asn Ala Trp Thr Pro Ser Asn Asp Asp Asn Pro Trp Ile			
115	120	125	
Gln Val Asn Leu Leu Arg Arg Met Trp Val Thr Gly Val Val Thr Gln			
130	135	140	
Gly Ala Ser Arg Leu Ala Ser His Glu Tyr Leu Lys Ala Phe Lys Val			
145	150	155	160
Ala Tyr Ser Leu Asn Gly His Glu Phe Asp Phe Ile His Asp Val Asn			
165	170	175	
Lys Lys His Lys Glu Phe Val Gly Asn Trp Asn Lys Asn Ala Val His			
180	185	190	
Val Asn Leu Phe Glu Thr Pro Val Glu Ala Gln Tyr Val Arg Leu Tyr			
195	200	205	
Pro Thr Ser Cys His Thr Ala Cys Thr Leu Arg Phe Glu Leu Leu Gly			
210	215	220	
Cys Glu Leu Asn Gly Cys Ala Asn Pro Leu Gly Leu Lys Asn Asn Ser			
225	230	235	240
Ile Pro Asp Lys Gln Ile Thr Ala Ser Ser Ser Tyr Lys Thr Trp Gly			
245	250	255	
Leu His Leu Phe Ser Trp Asn Pro Ser Tyr Ala Arg Leu Asp Lys Gln			
260	265	270	
Gly Asn Phe Asn Ala Trp Val Ala Gly Ser Tyr Gly Asn Asp Gln Trp			
275	280	285	
Leu Gln Val Asp Leu Gly Ser Ser Lys Glu Val Thr Gly Ile Ile Thr			
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Gln Gly Ala Arg Asn Phe Gly Ser Val Gln Phe Val Ala Ser Tyr Lys			
305	310	315	320
Val Ala Tyr Ser Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro			
325	330	335	
Arg Thr Gly Ser Ser Lys Ile Phe Pro Gly Asn Trp Asp Asn His Ser			
340	345	350	
His Lys Lys Asn Leu Phe Glu Thr Pro Ile Leu Ala Arg Tyr Val Arg			
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<213> mammalian

<220>

<221> CDS

<222> (46)..(1434)

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Arg Val Leu Ala Ala Leu Cys Gly Met Leu Leu Cys Ala Ser Gly Leu  
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ttc gcc gcg tct ggt gac ttc tgt gac tcc agc ctg tgc ctg aac ggt 153  
Phe Ala Ala Ser Gly Asp Phe Cys Asp Ser Ser Leu Cys Leu Asn Gly  
25 30 35

ggc acc tgc ttg acg ggc caa gac aat gac atc tac tgc ctc tgc cct 201  
Gly Thr Cys Leu Thr Gly Gln Asp Asn Asp Ile Tyr Cys Leu Cys Pro  
40 45 50

gaa ggc ttc aca ggc ctt gtg tgc aat gag act gag aga gga cca tgc 249  
Glu Gly Phe Thr Gly Leu Val Cys Asn Glu Thr Glu Arg Gly Pro Cys  
55 60 65

tcc cca aac cct tgc tac aat gat gcc aaa tgt ctg gtg act ttg gac 297  
Ser Pro Asn Pro Cys Tyr Asn Asp Ala Lys Cys Leu Val Thr Leu Asp  
70 75 80

aca cag cgt ggg gac atc ttc acc gaa tac atc tgc cag tgc cct gtg 345  
Thr Gln Arg Gly Asp Ile Phe Thr Glu Tyr Ile Cys Gln Cys Pro Val  
85 90 95 100

ggc tac tcg ggc atc cac tgt gaa acc gag acc aac tac tac aac ctg 393  
Gly Tyr Ser Gly Ile His Cys Glu Thr Glu Thr Asn Tyr Tyr Asn Leu  
105 110 115

gat gga gaa tac atg ttc acc aca gcc gtc ccc aat act gcc gtc ccc 441  
Asp Gly Glu Tyr Met Phe Thr Thr Ala Val Pro Asn Thr Ala Val Pro  
120 125 130

acc ccg gcc ccc acc ccc gat ctt tcc aac aac cta gcc tcc cgt tgt 489  
Thr Pro Ala Pro Thr Pro Asp Leu Ser Asn Asn Leu Ala Ser Arg Cys  
135 140 145

tct aca cag ctg ggc atg gaa ggg ggc gcc att gct gat tca cag att 537  
Ser Thr Gln Leu Gly Met Glu Gly Gly Ala Ile Ala Asp Ser Gln Ile  
150 155 160

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Ser Ala Ser Tyr Val Tyr Met Gly Phe Met Gly Leu Gln Arg Trp Gly

165	170	175	180	
ccg gag ctg gct cgt ctg tac cgc aca ggg atc gtc aat gcc tgg cac	633			
Pro Glu Leu Ala Arg Leu Tyr Arg Thr Gly Ile Val Asn Ala Trp His				
185	190	195		
gcc agc aac tat gat agc aag ccc tgg atc cag gtg aac ctt ctg cgg	681			
Ala Ser Asn Tyr Asp Ser Lys Pro Trp Ile Gln Val Asn Leu Leu Arg				
200	205	210		
aag atg cgg gta tca ggt gtg atg acg cag ggt gcc agc cgt gcc ggg	729			
Lys Met Arg Val Ser Gly Val Met Thr Gln Gly Ala Ser Arg Ala Gly				
215	220	225		
agg gcg gag tac ctg aag acc ttc aag gtg gct tac agc ctc gac gga	777			
Arg Ala Glu Tyr Leu Lys Thr Phe Lys Val Ala Tyr Ser Leu Asp Gly				
230	235	240		
cgc aag ttt gag ttc atc cag gat gaa agc ggt gga gac aag gag ttt	825			
Arg Lys Phe Glu Phe Ile Gln Asp Glu Ser Gly Gly Asp Lys Glu Phe				
245	250	255	260	
ttg ggt aac ctg gac aac aac agc ctg aag gtt aac atg ttc aac ccg	873			
Leu Gly Asn Leu Asp Asn Asn Ser Leu Lys Val Asn Met Phe Asn Pro				
265	270	275		
act ctg gag gca cag tac ata agg ctg tac cct gtt tcg tgc cac cgc	921			
Thr Leu Glu Ala Gln Tyr Ile Arg Leu Tyr Pro Val Ser Cys His Arg				
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Gly Cys Thr Leu Arg Phe Glu Leu Leu Gly Cys Glu Leu His Gly Cys				
295	300	305		
ctc gag ccc ctg ggc ctg aag aat aac aca att cct gac agc cag atg	1017			
Leu Glu Pro Leu Gly Leu Lys Asn Asn Thr Ile Pro Asp Ser Gln Met				
310	315	320		
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Ser Ala Ser Ser Ser Tyr Lys Thr Trp Asn Leu Arg Ala Phe Gly Trp				
325	330	335	340	
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Tyr Pro His Leu Gly Arg Leu Asp Asn Gln Gly Lys Ile Asn Ala Trp				
345	350	355		
acg gct cag agc aac agt gcc aag gaa tgg ctg cag gtt gac ctg ggc	1161			
Thr Ala Gln Ser Asn Ser Ala Lys Glu Trp Leu Gln Val Asp Leu Gly				
360	365	370		
act cag agg caa gtg aca gga atc atc acc cag ggg gcc cgt gac ttt	1209			
Thr Gln Arg Gln Val Thr Gly Ile Ile Thr Gln Gly Ala Arg Asp Phe				
375	380	385		

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 Gly His Ile Gln Tyr Val Glu Ser Tyr Lys Val Ala His Ser Asp Asp  
 390 395 400

ggt gtg cag tgg act gta tat gag gag caa gga agc agc aag gtc ttc 1305  
 Gly Val Gln Trp Thr Val Tyr Glu Glu Gln Gly Ser Ser Lys Val Phe  
 405 410 415 420

cag ggc aac ttg gac aac aac tcc cac aag aag aac atc ttc gag aaa 1353  
 Gln Gly Asn Leu Asp Asn Asn Ser His Lys Lys Asn Ile Phe Glu Lys  
 425 430 435

ccc ttc atg gct cgc tac gtg cgt gtc ctt cca gtg tcc tgg cat aac 1401  
 Pro Phe Met Ala Arg Tyr Val Arg Val Leu Pro Val Ser Trp His Asn  
 440 445 450

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 455 460

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Cys Leu Cys Pro Glu Gly Phe Thr Gly Leu Val Cys Asn Glu Thr Glu  
 50 55 60

Arg Gly Pro Cys Ser Pro Asn Pro Cys Tyr Asn Asp Ala Lys Cys Leu  
 65 70 75 80

Val Thr Leu Asp Thr Gln Arg Gly Asp Ile Phe Thr Glu Tyr Ile Cys  
 85 90 95

Gln Cys Pro Val Gly Tyr Ser Gly Ile His Cys Glu Thr Glu Thr Asn  
 100 105 110

Tyr Tyr Asn Leu Asp Gly Glu Tyr Met Phe Thr Thr Ala Val Pro Asn  
 115 120 125

Thr Ala Val Pro Thr Pro Ala Pro Thr Pro Asp Leu Ser Asn Asn Leu  
 130 135 140

Ala Ser Arg Cys Ser Thr Gln Leu Gly Met Glu Gly Gly Ala Ile Ala  
 145 150 155 160

Asp Ser Gln Ile Ser Ala Ser Tyr Val Tyr Met Gly Phe Met Gly Leu  
 165 170 175

Gln Arg Trp Gly Pro Glu Leu Ala Arg Leu Tyr Arg Thr Gly Ile Val  
 180 185 190

Asn Ala Trp His Ala Ser Asn Tyr Asp Ser Lys Pro Trp Ile Gln Val  
 195 200 205

Asn Leu Leu Arg Lys Met Arg Val Ser Gly Val Met Thr Gln Gly Ala  
 210 215 220

Ser Arg Ala Gly Arg Ala Glu Tyr Leu Lys Thr Phe Lys Val Ala Tyr  
 225 230 235 240

Ser Leu Asp Gly Arg Lys Phe Glu Phe Ile Gln Asp Glu Ser Gly Gly  
 245 250 255

Asp Lys Glu Phe Leu Gly Asn Leu Asp Asn Asn Ser Leu Lys Val Asn  
 260 265 270

Met Phe Asn Pro Thr Leu Glu Ala Gln Tyr Ile Arg Leu Tyr Pro Val  
 275 280 285

Ser Cys His Arg Gly Cys Thr Leu Arg Phe Glu Leu Leu Gly Cys Glu  
 290 295 300

Leu His Gly Cys Leu Glu Pro Leu Gly Leu Lys Asn Asn Thr Ile Pro  
 305 310 315 320



Asp Ser Gln Met Ser Ala Ser Ser Ser Tyr Lys Thr Trp Asn Leu Arg  
 325 330 335

Ala Phe Gly Trp Tyr Pro His Leu Gly Arg Leu Asp Asn Gln Gly Lys  
 340 345 350

Ile Asn Ala Trp Thr Ala Gln Ser Asn Ser Ala Lys Glu Trp Leu Gln  
 355 360 365

Val Asp Leu Gly Thr Gln Arg Gln Val Thr Gly Ile Ile Thr Gln Gly  
 370 375 380

Ala Arg Asp Phe Gly His Ile Gln Tyr Val Glu Ser Tyr Lys Val Ala  
 385 390 395 400

His Ser Asp Asp Gly Val Gln Trp Thr Val Tyr Glu Glu Gln Gly Ser  
 405 410 415

Ser Lys Val Phe Gln Gly Asn Leu Asp Asn Asn Ser His Lys Lys Asn  
 420 425 430

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:oligonucleotide

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<210> 6

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:oligonucleotide

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